

Sequence Comparison A

SEQ ID NO: 1

RESULT 1
 US-08-084-848A-13
 ; Sequence 13, Application US/08084848A
 ; Patent No. 5432155
 ; GENERAL INFORMATION:
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: Rivier, Jean E. F.
 ; APPLICANT: Cruz, Lourdes J.
 ; APPLICANT: Abogadie, Fe
 ; APPLICANT: Hopkins, Chris E.
 ; APPLICANT: Dykert, John
 ; APPLICANT: Torres, Josep L.
 ; TITLE OF INVENTION: Conotoxins I
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fitch, Even, Tabin & Flannery
 ; STREET: 135 South LaSalle Street, Suite 900
 ; CITY: Chicago
 ; STATE: Illinios
 ; COUNTRY: USA
 ; ZIP: 60603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/084,848A
 ; FILING DATE: June 29, 1993
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Schumann,, James J.
 ; REGISTRATION NUMBER: 20856
 ; REFERENCE/DOCKET NUMBER: 52511
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619)552-1311
 ; TELEFAX: (619)552-0095
 ; TELEX: 20 6566 PATLAW CGO
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 US-08-084-848A-13

Query Match 94.4%; Score 68; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 1.6e-06;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SEEGGSNATKKXYIL 16
 |||||
 Db 2 SEEGGSNATKKPYIL 16

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	"5700778".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:26
L2	0	craig-grey-a.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:26
L3	7	craig-a-grey.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:26
L4	13	griffin-david.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:26
L5	85	olivera-baldomero-m.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:27
L6	41	hillyard-david-r.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:27
L7	6	imperial-julita.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:27
L8	34	cruz-lourdes-j.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:27
L9	10	wagstaff-john-d.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:28
L10	20	layer-richard-t.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:28
L11	90	jones-robert-m.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:28
L12	25	mccabe-r-tyler.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:28

L13	21	contulakin same peptide	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:29
L14	2	"6369193".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:29
L15	2	"6344551".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:29
L16	2	"6696408".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/26 10:29

10067857 Results

SEQ ID NO: 1

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	68	94.4		16	16	R70723	New class of conot
2	40	55.6		1268	18	W58774	Human breast cance
3	40	55.6		1315	21	Y84046	Splice variant of
4	40	55.6		1353	21	Y84045	Splice variant of
5	40	55.6		1405	21	Y84044	Amino acid sequenc
6	40	55.6		1794	21	Y84040	Amino acid sequenc
7	39	54.2		884	17	W00160	MEI2 protein kinas
8	37	51.4		662	19	W81502	Dead Box X (DBX) g
9	37	51.4		662	19	W81501	Dead Box X (DBX) g
10	36	50.0		510	20	Y09184	Soybean cytochrome
11	36	50.0		614	19	W30682	Glycerol-3-phospha
12	36	50.0		614	19	W60257	Klebsiella pneumon
13	36	50.0		614	19	W57326	Mitochondrial glyc
14	36	50.0		614	20	Y26168	Mitochondrial glyc
15	36	50.0		863	21	Y87648	H. pylori outer me

SUMMARIES

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1	68	94.4		16	16	R70723	New class of conot
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3	40	55.6		1315	21	Y84046	Splice variant of
4	40	55.6		1353	21	Y84045	Splice variant of
5	40	55.6		1405	21	Y84044	Amino acid sequenc
6	40	55.6		1794	21	Y84040	Amino acid sequenc
7	39	54.2		884	17	W00160	MEI2 protein kinas
8	37	51.4		662	19	W81502	Dead Box X (DBX) g
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10	36	50.0		510	20	Y09184	Soybean cytochrome
11	36	50.0		614	19	W30682	Glycerol-3-phospha
12	36	50.0		614	19	W60257	Klebsiella pneumon
13	36	50.0		614	19	W57326	Mitochondrial glyc
14	36	50.0		614	20	Y26168	Mitochondrial glyc
15	36	50.0		863	21	Y87648	H. pylori outer me
16	36	50.0		877	19	W98214	H. pylori GHPO 108
17	36	50.0		934	17	R92289	Cycloisomaltooligo
18	36	50.0		972	17	R92288	Cycloisomaltooligo
19	36	50.0		972	20	Y32761	Bacillus CITase pr

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	68	94.4		16	1	US-08-084-848A-13	Sequence 13, Appl
2	68	94.4		16	1	US-08-458-499-13	Sequence 13, Appl
3	37	51.4		662	3	US-09-058-489-15	Sequence 15, Appl
4	37	51.4		662	3	US-09-058-489-16	Sequence 16, Appl
5	36	50.0		510	3	US-08-948-564-4	Sequence 4, Appli
6	36	50.0		614	3	US-08-968-563-13	Sequence 13, Appl
7	36	50.0		614	3	US-08-969-683A-13	Sequence 13, Appl
8	35	48.6		16	1	US-07-942-245-110	Sequence 110, App
9	35	48.6		131	3	US-09-208-804-1	Sequence 1, Appli
10	35	48.6		131	3	US-08-801-743-1	Sequence 1, Appli
11	35	48.6		145	1	US-08-470-179-32	Sequence 32, Appl
12	35	48.6		361	1	US-07-946-497-6	Sequence 6, Appli

13	35	48.6	361	1	US-08-483-322-6	Sequence 6, Appli
14	35	48.6	361	2	US-08-478-882-6	Sequence 6, Appli
15	35	48.6	599	1	US-07-879-617A-10	Sequence 10, Appl
16	35	48.6	599	1	US-08-295-814E-11	Sequence 11, Appl
17	35	48.6	599	1	US-08-240-783B-4	Sequence 4, Appli

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	68	94.4	76	2	A59043	contulakin-G precu
2	41	56.9	328	1	JN0642	naphthalene 1,2-di
3	40	55.6	660	2	A32378	probable ATP-depen
4	40	55.6	1254	2	JC7185	chromosome 1 Clorf
5	39	54.2	907	2	T48500	Mei2-like protein
6	38	52.8	433	2	T31511	hypothetical prote
7	38	52.8	512	2	T47554	cytochrome P450 ho
8	37	51.4	364	2	G71410	probable protein k
9	37	51.4	580	2	T40867	aspartate--tRNA li
10	37	51.4	662	1	I84741	RNA helicase - mou
11	36	50.0	67	2	B72248	ribosomal protein
12	36	50.0	218	2	S73626	MG364 homolog Gl2_
13	36	50.0	373	2	T26685	hypothetical prote
14	36	50.0	426	2	T39431	probable methionin
15	36	50.0	510	2	T05939	cytochrome P450 mo
16	36	50.0	589	2	S33920	beta-fructofuranos

Result No.	Score	% Match	Query Length	DB	ID	Description
1	68	94.4	76	5	Q9XYR5	Q9xyr5 conus geogr
2	40	55.6	1254	4	Q9UBS9	Q9ubs9 homo sapien
3	40	55.6	1405	4	Q9UL04	Q9ul04 homo sapien
4	39	54.2	403	12	O41569	O41569 human immun
5	39	54.2	777	4	Q9UH84	Q9uh84 homo sapien
6	39	54.2	859	12	O41567	O41567 human immun
7	39	54.2	884	10	O23866	O23866 arabidopsis
8	39	54.2	907	10	Q9LYN7	Q9lyn7 arabidopsis
9	38	52.8	116	2	Q9RPP5	Q9rpp5 ehrlichia c
10	38	52.8	433	5	Q9U2T2	Q9u2t2 caenorhabdi
11	38	52.8	512	10	Q9LF95	Q9lf95 arabidopsis
12	37	51.4	278	12	Q65460	Q65460 bovine vira
13	37	51.4	364	10	O23334	O23334 arabidopsis
14	37	51.4	385	10	Q39216	Q39216 arabidopsis
15	37	51.4	580	3	O74407	O74407 schizosacch
16	37	51.4	627	12	Q65811	Q65811 mucosal dis
17	37	51.4	1075	5	Q9NGP8	Q9ngp8 drosophila
18	37	51.4	1107	10	Q9ZUL9	Q9zul9 arabidopsis

SEQ ID NO: 2

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	17	53.1	110	17	R99961	Cladosporium herba
2	17	53.1	252	19	W64659	Mistletoe rMLA pro
3	17	53.1	252	19	W64661	Mistletoe rMLA var
4	17	53.1	253	18	W10022	Prepro mistletoe l
5	17	53.1	253	20	W90125	Mistletoe ML A-cha
6	17	53.1	254	20	Y25980	Mistletoe lectin A
7	17	53.1	254	20	Y25983	Mistletoe lectin A
8	17	53.1	256	20	Y25981	Mistletoe lectin A
9	17	53.1	256	20	Y25984	Mistletoe lectin A
10	17	53.1	494	20	Y34615	Chlamydia pneumoni
11	17	53.1	531	20	Y25979	Mistletoe lectin I

12	17	53.1	532	20	Y25982	Mistletoe lectin I
13	17	53.1	550	20	Y34807	C. pneumoniae prot
14	17	53.1	561	20	Y36997	Chlamydia trachoma
15	17	53.1	564	18	W10021	Prepro mistletoe l
16	17	53.1	564	20	W90127	Mistletoe lectin p
17	17	53.1	945	20	W88428	Chlamydia pneumoni

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	16	50.0	104	1	US-08-716-588-1	Sequence 1, Appli
2	16	50.0	104	2	US-08-966-444-1	Sequence 1, Appli
3	16	50.0	112	3	US-09-142-469-5	Sequence 5, Appli
4	16	50.0	233	1	US-08-518-223-5	Sequence 5, Appli
5	16	50.0	297	2	US-08-859-106A-2	Sequence 2, Appli
6	16	50.0	297	3	US-09-142-469-2	Sequence 2, Appli
7	16	50.0	352	3	US-09-108-020-14	Sequence 14, Appl
8	16	50.0	352	3	US-09-108-020-51	Sequence 51, Appl
9	16	50.0	373	1	US-07-723-002C-2	Sequence 2, Appli
10	16	50.0	383	5	5470718-5	Patent No. 5470718
11	16	50.0	388	1	US-08-499-568-11	Sequence 11, Appl
12	16	50.0	388	2	US-08-793-958-11	Sequence 11, Appl
13	16	50.0	392	2	US-08-904-031-1	Sequence 1, Appli
14	16	50.0	393	1	US-08-220-151-23	Sequence 23, Appl
15	16	50.0	393	1	US-08-413-118-23	Sequence 23, Appl

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	18	56.2	453	2	A69494	Glu-tRNA amidotran
2	17	53.1	129	2	F72488	hypothetical prote
3	17	53.1	140	2	A57544	BM88 antigen - pig
4	17	53.1	157	2	S49448	oleosin - rape
5	17	53.1	165	2	S50195	oleosin - rape
6	17	53.1	202	2	T01510	hypothetical prote
7	17	53.1	242	2	A75023	hypothetical prote
8	17	53.1	243	2	G71209	hypothetical prote
9	17	53.1	254	2	PD0018	mistletoe lectin I
10	17	53.1	339	2	T37470	seven-in-absentia
11	17	53.1	384	2	A69552	3-ketoacyl-CoA thi
12	17	53.1	469	2	D72722	probable MRSA prot
13	17	53.1	519	2	T14639	cytochrome P450 CY
14	17	53.1	550	2	A72106	pyrophosphate--fru
15	17	53.1	553	2	G71543	probable fructose-
16	17	53.1	553	2	C81698	pyrophosphate--fru
17	17	53.1	582	2	S74819	extracellular solu
18	17	53.1	605	2	A27274	ribophorin I precu
19	17	53.1	610	2	T22687	hypothetical prote
20	17	53.1	1282	2	T30577	DNA topoisomerase
21	17	53.1	2723	2	T03221	probable polyketid
22	16	50.0	28	2	F54346	pyruvate synthase

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	18	56.2	453	1	YJ54_ARCFU	O28325 archaeoglob
2	17	53.1	110	1	RLA1_CLAHE	P50344 cladosporiu
3	17	53.1	140	1	BM88_PIG	Q29026 sus scrofa
4	17	53.1	166	1	YNT5_ANASP	Q05070 anabaena sp
5	17	53.1	254	1	MLA_VISAL	P81446 viscum albu
6	17	53.1	349	1	F16P_RHIME	P56886 rhizobium m
7	17	53.1	519	1	CP99_SORBI	O48957 sorghum bic

8	17	53.1	605	1	RIB1_RAT	P07153 rattus norv
9	17	53.1	1282	1	TP2M_DICDI	P90520 dictyosteli
10	16	50.0	178	1	PORC_METJA	Q57717 methanococc
11	16	50.0	180	1	PORC_METTH	O27772 methanobact
12	16	50.0	185	1	PORC_PYRFU	Q51799 p pyruvate/
13	16	50.0	185	1	PORC_PYRHO	O58411 p pyruvate/
14	16	50.0	200	1	Y690_METJA	Q58102 methanococc
15	16	50.0	219	1	YOPE_YEREN	P31492 yersinia en
16	16	50.0	219	1	YOPE_YERPE	P31493 yersinia pe
17	16	50.0	219	1	YOPE_YERPS	P08008 yersinia ps

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	19	59.4	322	4	Q14968	Q14968	homo sapien
2	19	59.4	815	10	Q9LWL0	Q9LWL0	oryza sativ
3	18	56.2	128	13	P70094	P70094	xenopus lae
4	18	56.2	1232	10	Q9LJQ1	Q9LJQ1	arabidopsis
5	17	53.1	82	12	Q9Q3H2	Q9Q3H2	hepatitis c
6	17	53.1	129	1	Q9Y8T4	Q9Y8T4	aeropyrum p
7	17	53.1	141	5	Q9VZV5	Q9VZV5	drosophila
8	17	53.1	157	10	Q39338	Q39338	brassica na
9	17	53.1	165	10	Q39352	Q39352	brassica na
10	17	53.1	191	12	Q9QCX2	Q9QCX2	chayote mos
11	17	53.1	202	10	O04712	O04712	arabidopsis
12	17	53.1	203	5	O61530	O61530	meloidogyne
13	17	53.1	242	1	Q9UXY9	Q9UXY9	pyrococcus
14	17	53.1	243	1	O59606	O59606	pyrococcus
15	17	53.1	263	2	O52551	O52551	amycolatops
16	17	53.1	325	8	Q9MUE2	Q9MUE2	nicotiana t